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#312
0366
DOCKET NO. CDS-0232



IN THE UNITED STATES
PATENT AND TRADEMARK OFFICE

Applicant(s): John W. Sutherland

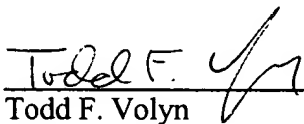
For: DETECTING NUCLEIC ACID DETECTION SEQUENCES

Filed: June 11, 2001

Serial No: 09/877,748

Verified Statement Under 37 CFR §1.821(f)

I hereby verify that the computer readable diskette enclosed herewith includes the same information as provided in the Sequence Listing of the subject application, and that this statement is made with the knowledge that willful false statements and the like so made are punishable by fine or imprisonment or both, under Section 1001 of the Title 18 of the United States Code and that willful false statements may jeopardize the validity of the application or any patent issued thereon.



Todd F. Volyn

Reg. No. 37,463

Dated: January 14, 2002

Johnson & Johnson

One New Brunswick Plaza 08933-7003

New Brunswick, NJ

DISK TO STIC

DATE: _____





SYSTEMS
BRANCH

CRF Problem Report

The Scientific and Technical Information Center (STIC) experienced a problem when processing the following computer readable form (CRF):

Application Serial Number: 09/877,748

Filing Date: 6-11-01

Date Processed by STIC: 6-28-01

STIC Contact: Mark Spencer, 703-308-4212

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Nature of Problem:

The CRF (was):

☐ (circle one) Damaged or Unreadable (for Unreadable, see attached)

☐ Blank (no files on CRF) (see attached)

☐ Empty file (filename present, but no bytes in file) (see attached)

☐ Virus-infected. Virus name: _____ The STIC will not process the CRF.

☐ Not saved in ASCII text

☐ Sequence Listing was embedded in the file. According to Sequence Rules, submitted file should **only** be the Sequence Listing.

☐ Did not contain a Sequence Listing. (see attached sample)

☒ Other: Non valid sequence listing format.

**PLEASE USE THE CHECKER VERSION 3.0 PROGRAM TO REDUCE ERRORS.
SEE BELOW FOR DETAILS:**

Checker Version 3.0

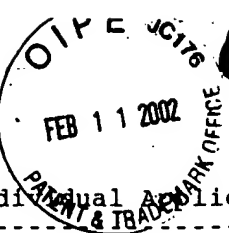
The Checker Version 3.0 application is a state-of-the-art Windows based software program employing a logical and intuitive user-interface to check whether a sequence listing is in compliance with format and content rules. Checker Version 3.0 works for sequence listings generated for the original version of 37 CFR §§1.821 - 1.825 effective October 1, 1990 (old rules) and the revised version (new rules) effective July 1, 1998 as well as World Intellectual Property Organization (WIPO) Standard ST.25.

Checker Version 3.0 replaces the previous DOS-based version of Checker, and is Y2K-compliant. Checker allows public users to check sequence listings in Computer Readable form (CRF) before submitting them to the United States Patent and Trademark Office (USPTO).

Use of Checker prior to filing the sequence listing is expected to result in fewer errored sequence listings, thus saving time and money.

Checker Version 3.0 can be down loaded from the USPTO website at the following address:

<http://www.uspto.gov/web/offices/pac/checker>



09/877,748

p.1

09/877,748

Individual Applicant

Street : 57 Culver Road
City : Rochester
State : New York
Country : USA
PostalCode : 14620-____
PhoneNumber : ____-____-____
FaxNumber : ____-____-____
EmailAddress :

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Does Not Comply
Corrected Diskette Needed

<110> LastName : Sutherland
<110> FirstName : John
<110> MiddleInitial : W
<110> Suffix :

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*Non valid sequence
listing format. See
attached example of
valid sequence listing
and explanation of
features.*

Individual Applicant

Street : 57 Culver Road
City : Rochester
State : New York
Country : USA
PostalCode : 14620-____
PhoneNumber : ____-____-____
FaxNumber : ____-____-____
EmailAddress :

<110> LastName : Sutherland
<110> FirstName : John
<110> MiddleInitial : W
<110> Suffix :

Application Project

<120> Title : Detecting Nucleic Acid Detection Sequences
<130> AppFileReference : CDS-232
<140> CurrentAppNumber :
<141> CurrentFilingDate : ____-____-____

Sequence

<213> OrganismName : Synthetic construct
<400> PreSequenceString :
cacagacatc ataacaaaaa atttcacca aacccccctt cccccgttc tggccacagc
60acttaaacac atctctgcc aacccccaaa acaaagaacc ctaacac
<212> Type : DNA
<211> Length : 107
SequenceName : First Sequence
SequenceDescription :

107

Custom Codon

Sequence Name : First Sequence



APPENDIX 3

SPECIMEN SEQUENCE LISTING

**COPY OF PAPERS
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<110> Smith, John; Smithgene Inc.

<120> Example of a Sequence Listing

<130> 01-00001

<140> PCT/EP98/00001

<141> 1998-12-31

<150> US 08/999,999

<151> 1997-10-15

<160> 4

<170> PatentIn version 2.0

<210> 1

<211> 389

<212> DNA

<213> Paramecium sp.

<220>

<221> CDS

<222> (279)...(389)

<300>

<301> Doe, Richard

<302> Isolation and Characterization of a Gene Encoding a
Protease from Paramecium sp.

<303> Journal of Genes

<304> 1

<305> 4

<306> 1-7

<307> 1988-06-31

<308> 123456

<309> 1988-06-31

<400> 1

agctgtagtc attcctgtgt cctcttctct ctgggcttct caccctgcta atcagatctc 60

agggagagtg tcttgaccct cctctgcctt tgcagcttca caggcaggca ggcaggcagc 120

tgatgtggca attgctggca gtgccacagg cttttcagcc aggccttaggg tgggttcgcg 180

cgcggcgcgg cggccctctt cgcgctcttc tcgcgctctt ctctcgtctt cctctcgtct 240

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ggacctgatt aggtgagcag gaggagggggg cagtttagc atg gtt tca atg ttc agc 296
Met Val Ser Met Phe Ser

ttg tct ttc aaa tgg cct gga ttt tgt ttg ttt gtt tgt ttg ttc caa 344
Leu Ser Phe Lys Trp Pro Gly Phe Cys Leu Phe Val Cys Leu Phe Gln

tgt ccc aaa gtc ctc ccc tgt cac tca tca ctg cag ccg aat ctt 389
Cys Pro Lys Val Leu Pro Cys His Ser Ser Leu Gln Pro Asn Leu

<210> 2
<211> 37
<212> PRT
<213> Paramecium sp.

<400> 2
Met Val Ser Met Phe Ser Leu Ser Phe Lys Trp Pro Gly Phe Cys Leu
1 5 10 15

Phe Val Cys Leu Phe Gln Cys Pro Lys Val Leu Pro Cys His Ser Ser
20 25 30

Leu Gln Pro Asn Leu
35

<210> 3
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> Designed peptide based on size and polarity to act as a linker between the alpha and beta chains of Protein XYZ.

<400> 3
Met Val Asn Leu Glu Pro Met His Thr Glu Ile
1 5 10

<210> 4
<400> 4
000

[Annex VIII follows]

<130>	Applicant	Preferably max. of 10 names; one name per line; preferable format: Surname, Other Names or Initials.	M. <i>Note</i>
<120>	Title of Invention		M.
<130>	File Reference	Personal file reference	M. when filed prior to assignment of appl. number.
<140>	Current Application Number	Specify as: US 07/999,999 or PCT/US96/99999	M, if available.
<141>	Current Filing Date	Specify as: yyyy-mm-dd	M, if available.
<150>	Prior Application Number	Specify as: US 07/999,999 or PCT/US96/99999	M, if applicable include priority documents under 35 USC 119 and 120.
<151>	Prior Application Filing Date	Specify as: yyyy-mm-dd	M, if applicable.
<160>	Number of SEQ ID NOs	Count includes total number of SEQ ID NOs	M.
<170>	Software	Name of software used to create the Sequence Listing.	O.
<210>	SEQ ID NO:1	Response shall be an integer representing the SEQ ID NO shown.	M.
<211>	Length	Respond with an integer expressing the number of bases or amino acid residues.	M.

Numeric Identifier	Definition	Comments and format	Mandatory (M) or optional (O).
<212>	Type	Whether presented sequence molecule is DNA, RNA, or PRT (protein). If a nucleotide sequence contains both DNA and RNA fragments, the type shall be "DNA." In addition, the combined DNA/RNA molecule shall be further described in the <220> to <223> feature section.	M.
<213>	Organism	Scientific name, i.e. Genus/ species, Unknown or Artificial Sequence. In addition, the "Unknown" or "Artificial Sequence" organisms shall be further described in the <220> to <223> feature section.	M.
<220>	Feature	Leave blank after <220>. <221-223> provide for a description of points of biological significance in the sequence.	M, under the following conditions: if "n," "Xaa," or a modified or unusual L-amino acid or modified base was used in a sequence; if ORGANISM is "Artificial Sequence" or "Unknown"; if molecule is combined DNA/RNA
<221>	Name/Key	Provide appropriate identifier for feature, preferably from WIPO Standard ST.25 (1990), Appendix 2, Tables 5 and 6.	M, under the following conditions: if "n," "Xaa," or a modified or unusual L-amino acid or modified base was used in a sequence.
<222>	Location	Specify location within sequence; where appropriate state number of first and last bases/ amino acids in feature.	M, under the following conditions: if "n," "Xaa," or a modified or unusual L-amino acid or modified base was used in a sequence.
<223>	Other Information	Other relevant information; four lines maximum	M, under the following conditions: if "n," "Xaa," or a modified or unusual L-amino acid or modified base was used in a sequence; if ORGANISM is "Artificial Sequence" or "Unknown"; if molecule is combined DNA/RNA.
<300>	Publication Information	Leave blank after <300>	O.
<301>	Authors	Preferably max of ten named authors of publication; specify one name per line; preferable format: Surname, Other Names and/or Initials.	O.
<302>	Title		O.
<303>	Journal		O.
<304>	Volume		O.
<305>	Issue		O.
<306>	Pages		O.
<307>	Date	Journal date on which data published; specify as yyyy-mm-dd, MMM-yyyy or Season-yyyy.	O.
<308>	Database Accession Number	Accession number assigned by database including database name.	O.
<309>	Database Entry Date	Date of entry in database; specify as yyyy-mm-dd or MMM-yyyy.	O.
<310>	Patent Document Number	Document number; for patent-type citations only. Specify as, for example, US 07/999,999.	O.
<311>	Patent Filing Date	Document filing date, for patent-type citations only; specify as yyyy-mm-dd.	O.
<312>	Publication Date	Document publication date, for patent-type citations only; specify as yyyy-mm-dd.	O.
<313>	Relevant Residues	FROM (position) TO (position)	O.
<400>	Sequence	SEQ ID NO should follow the numeric identifier and should appear on the line preceding the actual sequence.	M.